

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: DIXIT, VISHVA M.  
O'ROURKE, KAREN

(ii) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATING  
FAS-ASSOCIATED APOPTOSIS

(iii) NUMBER OF SEQUENCES: 10

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Morrison & Foerster
- (B) STREET: 755 Page Mill Road
- (C) CITY: Palo Alto
- (D) STATE: CA
- (E) COUNTRY: USA
- (F) ZIP: 94304-1018

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/443,982
- (B) FILING DATE: 18-MAY-1995
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Konski, Antoinette F.
- (B) REGISTRATION NUMBER: 34,202
- (C) REFERENCE/DOCKET NUMBER: 20344-21070.20

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (415) 813-5600
- (B) TELEFAX: (415) 494-0792
- (C) TELEX: 706141 MRSNFOERS SFO

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1642 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS

B1  
Control

(B) LOCATION: 130..756

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 4..6

(D) OTHER INFORMATION: /note= "An in-frame stop codon 130 base pairs upstream of the initiator methionine"

(ix) FEATURE:

- (A) NAME/KEY: polyA\_signal
- (B) LOCATION: 1636..1641

(D) OTHER INFORMATION: /note= "Potential poly(A) adenylation signal"

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 198..753

(D) OTHER INFORMATION: /note= "Clone-15; 5' end of FADD"

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 249..753

(D) OTHER INFORMATION: /note= "Clone-8; 5' end of FADD"

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 177..658

(D) OTHER INFORMATION: /note= "Death Domain of FADD"

(ix) FEATURE:

- (A) NAME/KEY: mutation

(B) LOCATION: replace(490..492, "aay")

(D) OTHER INFORMATION: /note= "For FADDmt: sequence is altered to either AAT or AAC and  
the codon from Val to Asn"

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature

(B) LOCATION: group(250..753, 232..753)

(D) OTHER INFORMATION: /note= "Codons can comprise C-terminal polypeptide fragments of FADD"

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature

(B) LOCATION: 253..753

(D) OTHER INFORMATION: /note= "Codons can comprise polypeptide fragment of FADD designated NFD-2"

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature

(B) LOCATION: 310..753

(D) OTHER INFORMATION: /note= "Codons can comprise polypeptide fragment of FADD designated NFD-3"

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 367..753

(D) OTHER INFORMATION: /note= "Codons can comprise polypeptide fragment of FADD designated NFD-4"

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 131..504

(D) OTHER INFORMATION: /note= "Codons can comprise an N-terminal half polypeptide fragment of FADD designated N-FADD"

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 133..501

(D) OTHER INFORMATION: /note= "Codons can comprise an N-terminal half polypeptide fragment of FADD"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCTAAAGGT TCGGGGGTGG AATCCTTGGG CCGCTGGGCA AGCGGCGAGA CCTGGCCAGG	60
GCCAGCGAGC CGAGGACAGA GGGCGCACGG AGGGCCGGGC CGCAGCCCCG GCCGCTTGCA	120
GACCCCGCC ATG GAC CCG TTC CTG GTG CTG CTG CAC TCG GTG TCG TCC	168
Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser	
1 5 10	
AGC CTG TCG AGC AGC GAG CTG ACC GAG CTC AAG TTC CTA TGC CTC GGG	216
Ser Leu Ser Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly	
15 20 25	
CGC GTG GGC AAG CGC AAG CTG GAG CGC GTG CAG AGC GGC CTA GAC CTC	264
Arg Val Gly Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu	
30 35 40 45	
TTC TCC ATG CTG CTG GAG CAG AAC GAC CTG GAG CCC GGG CAC ACC GAG	312
Phe Ser Met Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu	
50 55 60	
CTC CTG CGC GAG CTG CTC GCC TCC CTG CGG CGC CAC GAC CTG CTG CGG	360
Leu Leu Arg Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg	
65 70 75	
CGC GTC GAC GAC TTC GAG GCG GGG GCG GCG GCC GGG GCG CCT GGG	408
Arg Val Asp Asp Phe Glu Ala Gly Ala Ala Gly Ala Ala Pro Gly	
80 85 90	
GAA GAA GAC CTG TGT GCA GCA TTT AAC GTC ATA TGT GAT AAT GTG GGG	456
Glu Glu Asp Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly	
95 100 105	

AAA GAT TGG AGA AGG CTG GCT CGT CAG CTC AAA GTC TCA GAC ACC AAG Lys Asp Trp Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys 110 115 120 125	504
ATC GAC AGC ATC GAG GAC AGA TAC CCC CGC AAC CTG ACA GAG CGT GTG Ile Asp Ser Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val 130 135 140	552
CGG GAG TCA CTG AGA ATC TGG AAG AAC ACA GAG AAG GAG AAC GCA ACA Arg Glu Ser Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr 145 150 155	600
GTG GCC CAC CTG GTG GGG GCT CTC AGG TCC TGC CAG ATG AAC CTG GTG Val Ala His Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val 160 165 170	648
GCT GAC CTG GTA CAA GAG GTT CAG CAG GCC CGT GAC CTC CAG AAC AGG Ala Asp Leu Val Gln Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg 175 180 185	696
AGT GGG GCC ATG TCC CCG ATG TCA TGG AAC TCA GAC GCA TCT ACC TCC Ser Gly Ala Met Ser Pro Met Ser Trp Asn Ser Asp Ala Ser Thr Ser 190 195 200 205	744
GAA GCG TCC TGA TGGGCCGCTG CTTTGCCTG GTGGACCACA GGCATCTACA Glu Ala Ser *	796
CAGCCTGGAC TTTGGTTCTC TCCAGGAAGG TAGCCCAGCA CTGTGAAGAC CCAGCAGGAA	856
GCCAGGCTGA GTGAGCCACA GACCACCTGC TTCTGAACTC AAGCTGCCTT TATTAATGCC	916
TCTCCCGCAC CAGGCCGGGC TTGGCCCTG CACAGATATT TCCATTCTT CCTCACTATG	976
ACACTGAGCA AGATCTTGTCA TCCACTAAAT GAGCTCCTGC GGGAGTAGTT GGAAAGTTGG	1036
AACCGTGTCC AGCACAGAAG GAATCTGTGC AGATGAGCAG TCACACTGTT ACTCCACAGC	1096
GGAGGAGACC AGCTCAGAGG CCCAGGAATC GGAGCGAAGC AGAGAGGTGG AGAACTGGGA	1156
TTTGAACCCC CGCCATCCTT CACCAGAGCC CATGCTAAC CACTGTGGCG TTCTGCTGCC	1216
CCTGCAGTTG GCAGAAAGGA TGTTTGTCC CATTTCCTTG GAGGCCACCG GGACAGACCT	1276
GGACACTAGG GTCAGGCGGG GTGCTGTGGT GGGGAGAGGC ATGGCTGGGG TGGGGGTGGG	1336
GAGACCTGGT TGGCCGTGGT CCAGCTCTTG GCCCCTGTGT GAGTTGAGTC TCCTCTCTGA	1396
GACTGCTAAG TAGGGCAGT GATGGTTGCC AGGACGAATT GAGATAATAT CTGTGAGGTG	1456
CTGATGAGTG ATTGACACAC AGCACTCTCT AAATCTTCCT TGTGAGGATT ATGGGTCTCG	1516
CAATTCTACA GTTTCTTACT GTTTGTATC AAAATCACTA TCTTTCTGAT AACAGAATTG	1576

CCAAGGCAGC GGGATCTCGT ATCTTTAAAA AGCAGTCCTC TTATTCCCTAA GGTAATCCTA	1636
TTAAAAA	1642

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser Ser Leu Ser			
1	5	10	15
Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly Arg Val Gly			
20	25	30	
Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu Phe Ser Met			
35	40	45	
Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu Leu Leu Arg			
50	55	60	
Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg Arg Val Asp			
65	70	75	80
Asp Phe Glu Ala Gly Ala Ala Gly Ala Ala Pro Gly Glu Glu Asp			
85	90	95	
Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly Lys Asp Trp			
100	105	110	
Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys Ile Asp Ser			
115	120	125	
Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val Arg Glu Ser			
130	135	140	
Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr Val Ala His			
145	150	155	160
Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val Ala Asp Leu			
165	170	175	
Val Gln Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg Ser Gly Ala			
180	185	190	
Met Ser Pro Met Ser Trp Asn Ser Asp Ala Ser Thr Ser Glu Ala Ser			
195	200	205	

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(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 70 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /note= "Val is replaced by Asn for the point mutant hFADD"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Asp Trp Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys Ile  
1                       5                           10                       15

Asp Ser Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val Arg  
20                      25                           30

Glu Ser Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr Val  
35                      40                           45

Ala His Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val Ala  
50                      55                           60

Asp Leu Val Gln Glu Val  
65                      70

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 70 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /note= "Ile is replaced by Asn for the point mutant rFas"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Asp Ala Lys Lys Phe Ala Arg Gln His Lys Ile Pro Glu Ser Lys Ile  
1                   5                   10                   15  
  
Asp Glu Ile Glu His Asn Ser Pro Gln Asp Ala Ala Glu Gln Lys Ile  
20                  25                  30  
  
Gln Leu Leu Gln Cys Trp Tyr Gln Ser His Gly Lys Thr Gly Ala Cys  
35                  40                  45  
  
Gln Ala Leu Ile Gln Gly Leu Arg Lys Ala Asn Arg Cys Asp Ile Ala  
50                  55                  60  
  
Glu Glu Ile Gln Ala Met  
65                  70

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 70 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 11  
(D) OTHER INFORMATION: /note= "Val is replaced by Asn for  
the point mutant hFas"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Gln Val Lys Gly Phe Val Arg Lys Asn Gly Val Asn Glu Ala Lys Ile  
1               5               10               15  
  
Asp Glu Ile Lys Asn Asp Asn Val Gln Asp Thr Ala Glu Gln Lys Val  
20              25              30  
  
Gln Leu Leu Arg Asn Trp His Gln Leu His Gly Lys Glu Ala Tyr  
35              40              45  
  
Asp Thr Leu Ile Lys Asp Leu Lys Lys Ala Asn Leu Cys Thr Leu Ala  
50              55              60  
  
Glu Lys Ile Gln Thr Ile  
65              70

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 70 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site  
(B) LOCATION: 11  
(D) OTHER INFORMATION: /note= "Leu is replaced by Asn for  
the point mutant hTNFR-1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu Ile  
1 5 10 15

Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln Tyr  
20 25 30

Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala Thr  
35 40 45

Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly Cys  
50 55 60

Leu Glu Asp Ile Glu Glu  
65 70

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asp Thr Tyr Arg Tyr Ile  
1 5

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Asp Tyr Lys Asp Asp Asp Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 117 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AAGCCTGGTA CCATGCTGGG CATCTGGACC CTCCTACCTC TGGTTCTTAC GTCTGTTGCT

60

AGATTATCGT CCAAAGACTA CAAGGACGAC GATGACAAGA GTGTTAATGC CCAAGTC

117